

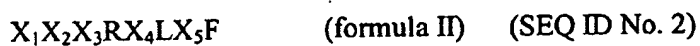
**Amendment to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

**1-15. (Cancelled)**

**16. (Previously Presented)** A peptide consisting of the formula;



wherein  $X_1$ ,  $X_3$ ,  $X_4$  and  $X_5$  are each a natural or unnatural amino acid and  $X_2$  is serine or alanine.

**17. (Original)** A peptide according to claim 16, wherein  $X_5$  is selected from isoleucine and glycine.

**18. (Original)** A peptide according to claim 16, wherein  $X_1$  and  $X_4$  are both basic amino acid residues and  $X_3$  is a basic or polar residue.

**19. (Original)** A peptide according to claim 18, wherein  $X_1$  is histidine and  $X_4$  is arginine, and  $X_3$  is lysine or cysteine.

**20. (Previously Presented)** A peptide consisting of the formula;

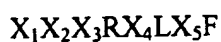


(SEQ ID No. 2)

wherein  $X_1$ ,  $X_3$ ,  $X_4$  and  $X_5$  are each a natural or unnatural amino acid and  $X_2$  is serine or alanine, wherein the peptide is

- (a) modified by deletion of one or more amino acid residues;
- (b) modified by substitution of one or more natural amino acid residues by the corresponding D-stereomer;
- (c) a cyclic;
- (d) modified by reversing the order of the final two residues at the C-terminal end;
- (e) any combination of (a)-(d).

**21. (Previously Presented)** A peptide consisting of the formula;



(SEQ ID No. 2)

wherein:

- (a)  $X_1$  is deleted or is a natural or unnatural amino acid,
- (b)  $X_2$  is serine or alanine or a straight or branched chain amino acid,
- (c)  $X_3$  is a basic amino acid or straight chain aliphatic amino acid,
- (d) R is unchanged or conservatively substituted by a basic amino acid,
- (e)  $X_4$  is an amino acid that is capable of providing at least one site for participating in hydrogen bonding,
- (f) L is unchanged or conservatively substituted,
- (g)  $X_5$  is a natural or unnatural amino acid, or
- (h) F is unchanged or substituted by an aromatic amino acid.

**22. (Previously Presented)** A peptide consisting of the formula;



(SEQ ID No. 2),

wherein

- (a)  $X_1$  is deleted or is a natural or unnatural amino acid residue,
- (b)  $X_2$  is a natural or unnatural amino acid residue having an aromatic or aliphatic side chain,
- (c)  $X_3$  is a basic residue, or an uncharged natural or unnatural amino acid residue,
- (d) arginine is replaced by a basic residue or an uncharged natural or unnatural amino acid residue,
- (e)  $X_4$  is a natural or unnatural amino acid residue, or an amino acid residue capable of forming a cyclic linkage,
- (f) leucine is replaced with a natural or unnatural amino acid residue having an aromatic or aliphatic side chain,
- (g)  $X_5$  is a natural or unnatural amino acid residue having an aromatic or aliphatic side chain,
- (h) phenylalanine is replaced with a natural or unnatural amino acid,
- (i)  $X_5$  and the terminal phenylalanine residue are reversed, or
- (j) the peptide is in cyclic form by the formation of a linkage between the side chain of  $X_4$  and the C-terminus residue.

**23. (Original)** A peptide according to claim 16, wherein  $X_2$  is alanine.

**24. (Previously Presented)** A peptide according to claim 16, wherein  $X_5$  is isoleucine.

**25. (Previously Presented) A peptide selected from the group consisting of:**

H S K R R L I F (SEQ ID No. 34)

H A K R R L I F (SEQ ID No. 35)

H S K R R L F G (SEQ ID No. 36)

H A K R R L F G (SEQ ID No. 37)

K A C R R L F G (SEQ ID No. 38)

K A C R R L I F (SEQ ID No. 39)

	X1	X2	X3	R	X4	L	X5	F	
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 28)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 40)
	H-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 41)
H-	Pyra-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 42)
H-	Thi-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 43)
H-	Hse-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 44)
H-	Phe-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 45)
H-	Dab-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 46)
H-	His-	Gly-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 47)
H-	His-	Abu-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 48)
H-	His-	Nva-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 49)
H-	His-	Bug-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 50)
H-	His-	Val-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 51)
H-	His-	Ile-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 52)
H-	His-	Phg-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 53)
H-	His-	Phe-	Lys-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 54)
H-	His-	Ala-	Ala-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 56)
H-	His-	Ala-	Nle-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 57)
H-	His-	Ala-	Abu-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 58)
H-	His-	Ala-	Leu-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 59)
H-	His-	Ala-	Arg-	Arg-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 60)
H-	His-	Ala-	Lys-	Ala-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 61)
H-	His-	Ala-	Lys-	Cit-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 62)
H-	His-	Ala-	Lys-	Hse-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 63)
H-	His-	Ala-	Lys-	His-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 64)
H-	His-	Ala-	Lys-	Nle-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 65)
H-	His-	Ala-	Lys-	Gln-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 66)
H-	His-	Ala-	Lys-	Lys-	Arg-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 67)
H-	His-	Ala-	Lys-	Arg-	Ala-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 68)
H-	His-	Ala-	Lys-	Arg-	Asn-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 69)
H-	His-	Ala-	Lys-	Arg-	Pro-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 70)
H-	His-	Ala-	Lys-	Arg-	Ser-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 71)
H-	His-	Ala-	Lys-	Arg-	Aib-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 72)

H-	His-	Ala-	Lys-	Arg-	Sar-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 73)
H-	His-	Ala-	Lys-	Arg-	Cit-	Leu-	Ile-	Phe	-NH2 (SEQ ID No. 74)
H-	His-	Ala-	Lys-	Arg-	Arg-	Ala-	Ile-	Phe	-NH2 (SEQ ID No. 76)
H-	His-	Ala-	Lys-	Arg-	Arg-	leu-	Ile-	Phe	-NH2 (SEQ ID No. 77)
H-	His-	Ala-	Lys-	Arg-	Arg-	Ile-	Ile-	Phe	-NH2 (SEQ ID No. 78)
H-	His-	Ala-	Lys-	Arg-	Arg-	Val-	Ile-	Phe	-NH2 (SEQ ID No. 79 )
H-	His-	Ala-	Lys-	Arg-	Arg-	Nlc-	Ile-	Phe	-NH2 (SEQ ID No. 80)
H-	His-	Ala-	Lys-	Arg-	Arg-	Nva-	Ile-	Phe	-NH2 (SEQ ID No. 81)
H-	His-	Ala-	Lys-	Arg-	Arg-	Cha-	Ile-	Phe	-NH2 (SEQ ID No. 82)
H-	His-	Ala-	Lys-	Arg-	Arg-	Phe-	Ile-	Phe	-NH2 (SEQ ID No. 83)
H-	His-	Ala-	Lys-	Arg-	Arg-	1Nap-	Ile-	Phe	-NH2 (SEQ ID No. 84)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ala-	Phe	-NH2 (SEQ ID No. 85)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Leu-	Phe	-NH2 (SEQ ID No. 86)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Val-	Phe	-NH2 (SEQ ID No. 87)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Nlc-	Phe	-NH2 (SEQ ID No. 88)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Nva-	Phe	-NH2 (SEQ ID No. 89)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Cha-	Phe	-NH2 (SEQ ID No. 90)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Phe-	Phe	-NH2 (SEQ ID No. 91)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	1Nap-	Phe	-NH2 (SEQ ID No. 92)
	H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Phe	-NH2 (SEQ ID No. 93)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Leu	-NH2 (SEQ ID No. 95)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Cha	-NH2 (SEQ ID No. 96)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Hof	-NH2 (SEQ ID No. 97)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Tyr	-NH2 (SEQ ID No. 98)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 99)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	mFPhe	-NH2 (SEQ ID No. 100)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Trp	-NH2 (SEQ ID No. 101)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	1Nap	-NH2 (SEQ ID No. 102)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	2Nap	-NH2 (SEQ ID No. 103)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Lys	-NH2 (SEQ ID No. 104)
H-	His-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Tic	-NH2 (SEQ ID No. 105)
H-	His	Ala	Lys	Arg	Arg	Leu	Ile	L-Pse	OH (SEQ ID No. 106)
H-	His	Ala	Lys	Arg	Arg	Leu	Ile	D-Pse	OH (SEQ ID No. 107)
H-	His	Ser	Lys	Arg	Arg	Leu	Ile	L-Pse	OH (SEQ ID No. 108)
H-	His	Ser	Lys	Arg	Arg	Leu	Ile	D-Pse	OH (SEQ ID No. 109)
H-	His	Ala	Lys	Arg	Arg	Leu	Ile	L-Psa	OH (SEQ ID No. 110)
H-	His	Ala	Lys	Arg	Arg	Leu	Ile	D-Psa	OH (SEQ ID No. 111)
H-	His	Ser	Lys	Arg	Arg	Leu	Ile	L-Psa	OH (SEQ ID No. 112)
H-	His	Ser	Lys	Arg	Arg	Leu	Ile	D-Psa	OH (SEQ ID No. 113)
H-	His	Ala	Lys	Arg	Arg	Leu	Ile	Dhp	OH (SEQ ID No. 114)
H-	His	Ser	Lys	Arg	Arg	Leu	Ile	Dhp	OH (SEQ ID No. 115)
H-	His	Ala	Lys	Arg	Arg	Leu	Ile	Pheol	(SEQ ID No. 116)
H-	His	Ser	Lys	Arg	Arg	Leu	Ile	Pheol	(SEQ ID No. 117)
H-	Ala-	Ala-	Abu-	Arg-	Arg-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 118)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 119)

H-	Ala-	Ala-	Lys-	Arg-	Cit-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 120)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ala-	pFPhe	-NH2 (SEQ ID No. 121)
H-	Ala-	Ala-	Abu-	Arg-	Ser-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 122)
H-	Ala-	Ala-	Lys-	Gln-	Arg-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 123)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 124)
H-	Gly-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 125)
H-	Ala-	Ala-	Lys-	hArg-	Arg-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 126)
H-	Ala-	Ala-	Lys-	Ser-	Arg-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 127)
H-	Ala-	Ala-	Lys-	Hse-	Arg-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 128)
H-	Ala-	Ala-	Lys-	Arg-	Lys-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 129)
H-	Ala-	Ala-	Lys-	Arg-	Om-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 130)
H-	Ala-	Ala-	Lys-	Arg-	Gln-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 131)
H-	Ala-	Ala-	Lys-	Arg-	Hse-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 132)
H-	Ala-	Ala-	Lys-	Arg-	Thr-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 133)
H-	Ala-	Ala-	Lys-	Arg-	Nva-	Leu-	Ile-	pFPhe	-NH2 (SEQ ID No. 134)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Phg-	Ile-	pFPhe	-NH2 (SEQ ID No. 135)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Met-	Ile-	pFPhe	-NH2 (SEQ ID No. 136)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Ala-	Ile-	pFPhe	-NH2 (SEQ ID No. 137)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Hof-	Ile-	pFPhe	-NH2 (SEQ ID No. 138)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	hLeu-	Ile-	pFPhe	-NH2 (SEQ ID No. 139)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	alle-	Ile-	pFPhe	-NH2 (SEQ ID No. 140)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Gly-	pFPhe	-NH2 (SEQ ID No. 141)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	βAla	pFPhe	-NH2 (SEQ ID No. 142)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Phg-	pFPhe	-NH2 (SEQ ID No. 143)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Aib-	pFPhe	-NH2 (SEQ ID No. 144)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Sar-	pFPhe	-NH2 (SEQ ID No. 145)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Pro-	pFPhe	-NH2 (SEQ ID No. 146)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Bug-	pFPhe	-NH2 (SEQ ID No. 147)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ser-	pFPhe	-NH2 (SEQ ID No. 148)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Asp-	pFPhe	-NH2 (SEQ ID No. 149)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Asn-	pFPhe	-NH2 (SEQ ID No. 150)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	pFPhe-	Phe	-NH2 (SEQ ID No. 151)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	diClPhe	Phe	-NH2 (SEQ ID No. 152)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	pClPhe-	Phe	-NH2 (SEQ ID No. 153)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	mClPhe	Phe	-NH2 (SEQ ID No. 154)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	oClPhe-	Phe	-NH2 (SEQ ID No. 155)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	pIPhe-	Phe	-NH2 (SEQ ID No. 156)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	TyrMe-	Phe	-NH2 (SEQ ID No. 157)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Thi-	Phe	-NH2 (SEQ ID No. 158)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Pya-	Phe	-NH2 (SEQ ID No. 159)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	diClPhe	-NH2 (SEQ ID No. 160)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	pClPhe	-NH2 (SEQ ID No. 161)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	mClPhe	-NH2 (SEQ ID No. 162)

H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	oClPhe	-NH <sub>2</sub>	(SEQ ID No. 163)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Phg	-NH <sub>2</sub>	(SEQ ID No. 164)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	TyrMe	-NH <sub>2</sub>	(SEQ ID No. 165)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Thi	-NH <sub>2</sub>	(SEQ ID No. 166)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Pya	-NH <sub>2</sub>	(SEQ ID No. 167)
H-	Ala-	Ala-	Lys-	Arg-	Arg-	Leu-	Ile-	Inc	-NH <sub>2</sub>	(SEQ ID No. 168)

and the cyclic peptides:

5,8-cyclo-[H-His-Ala-Lys-Arg-Lys-Leu-Phe-Gly] (SEQ ID No. 169)

5,8-cyclo-[H-His-Ala-Lys-Arg-Orn-Leu-Phe-Gly] (SEQ ID No. 170)

#### 26-35. (Cancelled)

**36. (Previously Presented)** An assay for the identification of compounds that interact with a cyclin or a cyclin when complexed with the physiologically relevant CDK, comprising;

(a) incubating a candidate compound and a peptide consisting of formula II

$X_1X_2X_3RX_4LX_5F$  (SEQ ID No. 2)

wherein  $X_1$ ,  $X_3$ ,  $X_4$  and  $X_5$  are each a natural or unnatural amino acid and  $X_2$  is serine or alanine and a cyclin or cyclin/CDK complex;

(b) detecting binding of either the candidate compound or the peptide of formula II with cyclin.

#### 37-40. (Cancelled)

**41. (Previously Presented)** An assay according to claim 36, wherein the cyclin is selected from cyclin A, cyclin E or cyclin D.

**42. (Original)** An assay according to claim 41 wherein the cyclin is cyclin A.

#### 43. (Cancelled)

**44. (Previously Presented)** An assay according to claim 36, wherein at least one of the assay components is bound to a solid phase.

- 45. (Original)** An assay according to claim 44, wherein the p21 derived peptide is labeled such as to emit a signal when bound to said cyclin.
- 46. (Original)** An assay according to claim 44, wherein the cyclin is labeled such as to emit a signal when bound to the p21 derived peptide.
- 47. (Original)** An assay according to claim 45, wherein one of the assay components is labeled with a fluorescence emitter and the signal is detected using fluorescence polarisation techniques.
- 48-54. (Cancelled)**
- 55. (Previously Presented)** A peptide according to claim 22, wherein  $X_1$  is selected from the group consisting of histidine, alanine, 3-pyraldylalanine (Pya), 2-thienylalanine (Thi), homoserine (Hse), phenylalanine and diaminobutyric acid (Dab).
- 56. (Previously Presented)** A peptide according to claim 22, wherein  $X_2$  is selected from the group consisting of alanine, glycine, aminobutyric acid (Abu), norvaline (Nva), t-butylglycine (Bug), valine, phenylglycine (Phg) and phenylalanine.
- 57. (Previously Presented)** A peptide according to claim 22, wherein  $X_3$  is selected from the group consisting of lysine, arginine, norleucine (Nle), aminobutyric acid (Abu) and leucine.
- 58. (Previously Presented)** A peptide according to claim 22, wherein arginine is replaced by lysine, citrulline (Cit), homoserine, histidine, norleucine (Nle) or glutamine.
- 59. (Previously Presented)** A peptide according to claim 22, wherein  $X_4$  is selected from the group consisting of arginine, asparagines, praline, serine, aminoisobutyric acid (Aib), sarcosine, lysine and ornithine.



- 60. (Previously Presented)** A peptide according to claim 22, wherein leucine is replaced by norleucine, norvaline, cyclohexylalanine (Cha), phenylalanine or 1-naphthylalanine (1Nal).
- 61. (Previously Presented)** A peptide according to claim 22, wherein  $X_5$  is selected from the group consisting of isoleucine, norleucine, norvaline, cyclohexylalanine (Cha), phenylalanine and 1-naphthylalanine (1Nal).
- 62. (Previously Presented)** A peptide according to claim 22, wherein phenylalanine is replaced by leucine, cyclohexylalanine (Cha), homophenylalanine (Hof), tyrosine, para-fluorophenylalanine (pFPhe), meta-fluorophenylalanine (mFPhe), tryptophan, i-naphthylalanine (1Nal), 2-naphthylalanine (2Nal), biphenylalanine (Bip) or (Tic).
- 63. (New)** The peptide of claim 20, wherein the peptide is modified by deletion of one or more amino acid residues.
- 64. (New)** The peptide of claim 20, wherein the peptide is modified by substitution of one or more natural amino acid residues by the corresponding D-stereomer.
- 65. (New)** The peptide of claim 20, wherein the peptide is a cyclic.
- 66. (New)** The peptide of claim 20, wherein the peptide is modified by reversing the order of the final two residues at the C-terminal end.
- 67. (New)** The peptide of claim 21, wherein  $X_1$  is deleted or is a natural or unnatural amino acid.
- 68. (New)** The peptide of claim 21, wherein  $X_2$  is serine or alanine or a straight or branched chain amino acid.

69. (New) The peptide of claim 21, wherein  $X_3$  is a basic amino acid or straight chain aliphatic amino acid.

70. (New) The peptide of claim 21, wherein R is unchanged or conservatively substituted by a basic amino acid.

71. (New) The peptide of claim 21, wherein  $X_4$  is an amino acid that is capable of providing at least one site for participating in hydrogen bonding.

72. (New) The peptide of claim 21, wherein L is unchanged or conservatively substituted.

73. (New) The peptide of claim 21, wherein  $X_5$  is a natural or unnatural amino acid.

74. (New) The peptide of claim 21, wherein F is unchanged or substituted by an aromatic amino acid.

75. (New) The peptide of claim 22, wherein  $X_1$  is deleted or is a natural or unnatural amino acid residue.

76. (New) The peptide of claim 22, wherein  $X_2$  is a natural or unnatural amino acid residue having an aromatic or aliphatic side chain.

77. (New) The peptide of claim 22, wherein  $X_3$  is a basic residue, or an uncharged natural or unnatural amino acid residue.

78. (New) The peptide of claim 22, wherein arginine is replaced by a basic residue or an uncharged natural or unnatural amino acid residue.

79. (New) The peptide of claim 22, wherein  $X_4$  is a natural or unnatural amino acid residue, or an amino acid residue capable of forming a cyclic linkage.

80. (New) The peptide of claim 22, wherein leucine is replaced with a natural or unnatural amino acid residue having an aromatic or aliphatic side chain.
81. (New) The peptide of claim 22, wherein  $X_5$  is a natural or unnatural amino acid residue having an aromatic or aliphatic side chain.
82. (New) The peptide of claim 22, wherein phenylalanine is replaced with a natural or unnatural amino acid.
83. (New) The peptide of claim 22, wherein  $X_5$  and the terminal phenylalanine residue are reversed.
84. (New) The peptide of claim 22, wherein the peptide is in cyclic form by the formation of a linkage between the side chain of  $X_4$  and the C-terminus residue.